

Sub
Fig

| | | | | |
|----------|---------------------|-------------------------------|-------------------|-------------|
| Notch(C) | IDE- SNP | QNGGT- - - D-VGSY- - - - - | GK- - - - - | CE-N |
| 10244(C) | -NECTM- - - | QOH- - - - | VNT- GSY- - - - - | Q- - - - - |
| 80 | | | CRCPGVT | GKT- - - - |
| 95 | VNECGMKPRP | QQR | Q | QSO D |
| 133 | VNSRTCAMIN | QYS | Q | QMP D |
| 175 | IDECASGKVI | CPYNRRC | VNTFGSYVCKCHIGEE | GLRLAPN |
| 220 | INECTMDSHT | CSHIANC | FNTQGSF | LOYISGR |
| | | | CKCHGK | QNGRLCS |
| CD27(C) | V- EC- SG- Q- - - - | SS- - - - | -NTVGSY- - - - - | PN- - - - |
| EGF(C) | NSDSECPPLSHDGYC | LDGVCMYTEALDKYACNVVGYI- - - - | GER- - - - | QYRDLKWWELR |

Figure 1

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACTGG
ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAAAGAAA
CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
CTTTTGCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAAGT
CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
(SEQ ID NO 1)

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACTGG
ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAAAGAAA
CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
CTTTTGCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAAGT
CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGAATCCGCC TGGCCCCAAA
TGGAAGAGAC TGTCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT
GTCCCTACAA TCGAAGATGT GTGAACACAT TTGGAAGCTA CTACTGCAAA
TGTCACATTG GTTTTCAACT GCAATATATC AGTGGACGAT ATGACTGTAT
AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA
ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT
AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA
AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG
CTCACAAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGTTACCCCA
GAACCCACCA GGAATCCTAC CCCTAAGGTG AACTTGCAGC CCTTCAACTA
TGAAGAGATA GTTTCCAGAG GCGGGAATC TCATGGAGGT AAAAAAGGGA
ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA
GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT
CCCTAAGGTG AATGAAGCAG GTGAATTCCG CCTGATTCTG GTCCAAAGGA
AAGCGTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTGGAC
TGCAGCTTCA ATCATGGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA
TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG
CAGTTCCGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAAACTT
CTCCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA
CCGGCTGGCC GGAGACAAAG TCGGGAAACT TCGAGTGTTT GTGAAAACA
GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAGAGTGG
AAGACAGGGA AAATTCAATT GTATCAAGGA ACTGATGCTA CCAAAAGCAT
CATTTTGAAG GCAGAACGTG GCAAGGGCAA AACCAGCGAA ATCGCAGTGG
ATGGCGTCTT GCTTGTTC GGTATATGTC CAGATAGCCT TTTATCTGTG
GANNNCTGAA TGGTACTATC TTTATATTTG ACTTTGTATG TCAGTTCCCT
GGTTTTTTTG ATATTGCATC ATAGGACCTC TGGCATTTTA AAATTACTAG
CTGAAAAATTG
(SEQ ID NO 2)

Figure 2

GWRNSKGVCEATCEPGCKFGECVGPNNKRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE
(SEQ ID NO 3)

GWRNSKGVCEATCEPGCKFGECVGPNNKRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP
NGRDCLDIDECASGKVICPYNRRVCNTFGSYCKCHIGFELQYISGRYDCIDINECTMDS
HTCSHHANCFNTQGSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH
KNSMKKKAKIKNVTPEPTRTPKVNLPFNYYEIVSRGGNSHGGKKGNEEKMKEGLE
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISVDCSF
NHGICDWKQDREDDFDWNPADRDNAGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN
FCLLFDYRLAGDKVVKLRVFKNSNNALAWKTTSEDEKWKTKIQLYQGTDATKSHF
EAERGKGKTGEIAVDGVLLVSGLCPSLLSVDDXMVLSLYLTLYVSSLVFLILHRTSGI
LKLLAEKL
(SEQ ID NO 4)

Figure 3

09627860-10300

00000000000000000000000000000000

(SEQ ID NO: 5)

Figure 5

(SEQ ID NO: 6)

(SEQ ID NO: 6)

EGFL6 (221-260 aa)

3D Model

EGF

NMR Structure

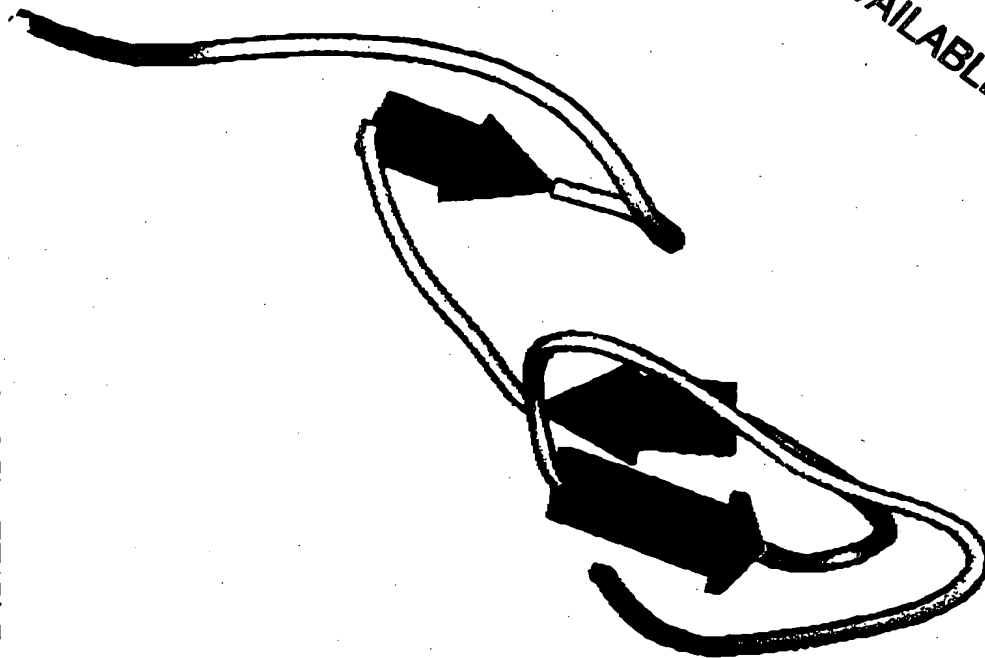
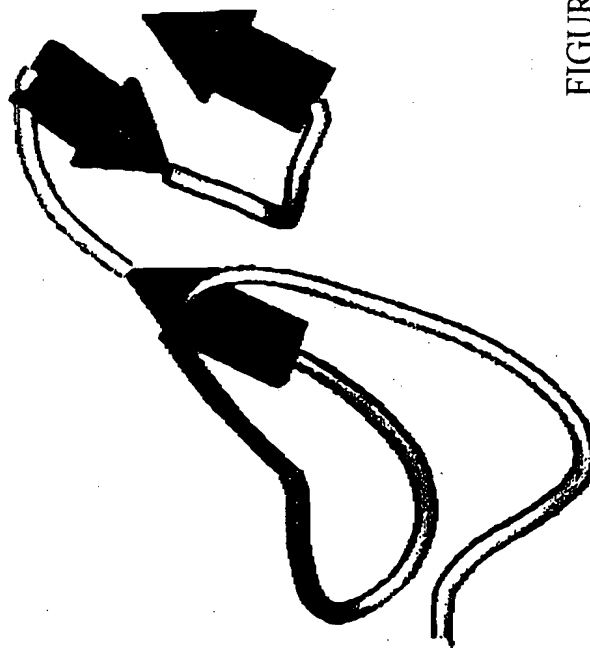


FIGURE 6

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